REMARKS

Claims 8-20 are active in this application. Support for Claims 12-20 is found in Claims 8-11 and the specification as originally filed. Support for the hybridization and 70% homology is found in the paragraph bridging pages 10-11. Support for the mutant DNA in Claim 17 is found in the specification on pages 9-10. The specification is amended to provide a sequence identifier for the sequence in Figure 2. No new matter is added by these amendments.

Applicants wish to thank Examiner Rao and Prouty for the courteous discussion granted to the Applicants' undersigned representative on March 5, 2003. During this meeting, various amendments were discussed to address the rejections of 35 U.S.C. § 112, first and second paragraphs, as well as the rejection over the prior art. These amendments are reflected in the claim amendments submitted herein.

Claims 8-11 have been rejected under 35 U.S.C. § 112, first paragraph, as not being adequately described nor enabled by the specification. These rejections are traversed for the following reasons.

Claim 8 provides a DNA coding for SEQ ID NO: 2. The specification describes the structure of the amino acid and based on that description one can readily envisage the structure of the DNA encoded therein. In addition, Applicants have described SEQ ID NO:1 as one of those structures. Therefore, Claims 8-11 are adequately described and enabled by the description provided in the specification.

With respect to the method in Claim 13, the DNA which is amplified to enhance homoserine resistance is one that hybridizes under stringent conditions to nucleotides 557 to 1171 of SEQ ID NO: 1, is not less than 70% homologous to SEQ ID NO: 1, and which has an activity of making the bacterium having the protein L-homoserine resistant. Provided with the nucleotide sequence in SEQ ID NO: 1 and the tools necessary to hybridize one DNA to

another DNA and determine whether it has the necessary homology and activity is within the well-described knowledge available in the art. In support of this knowledge, Applicants submit herewith a selected portion from "Short Protocols in Molecular Biology" unit 2.10, which describes hybridization analysis of DNA(third edition, Compendium of Methods From Current Protocols and Molecular Biology, Ausubel et al (eds.) John Wiley and Sons, Inc., New York). In addition, Applicants submit herewith a homology search with the rhtB sequence from *E. coli* using the BLAST and FASTA search engines as illustrative of the ability to ascertain the percent homology between two nucleotide sequences.

With respect to the written description portion of this rejection, Applicants respectfully direct the Examiner's attention to the U.S. PTO "Synopsis of Application of Written Description Guidelines" and, in particular, Example 9 (a copy is attached for reference).

In this Example a situation that is similar to Claim 13 is presented. The conclusion is that the claim in the Example, which is similar to Claim 13 in terms of providing for a sequence which hybridizes under stringent conditions to an allowable DNA, is adequately described. Thus, Claim 13 (and the claims dependent on Claim 13) is described because "a representative number of species is disclosed, since highly stringent hybridization conditions in combination with the coding function of DNA and the level of skill and knowledge in the art are adequate to determine that applicant was in possession of the claimed invention." (Example 9 of the "Synopsis").

Turning to Claim 17, the DNA of SEQ ID NO:1 is described. The methods of mutating and selecting the DNA with the activity of increasing homoserine resistance in the bacteria are described in the specification on page 9, line 4 to page 10, line 15. Therefore, Claim 17 (and the claims dependent thereon) meet the requirements of 35 U.S.C. § 112, first paragraph.

In light of the foregoing, Applicants respectfully request that the two rejections under 35 U.S.C. §112, first paragraph be withdrawn.

Turning to the rejections over the prior art, these rejections are traversed for the following reasons.

Claim 8 is drawn to a method for producing an amino acid wherein L-homoserine-resistance is enhanced by amplifying a copy of a DNA which codes for a protein comprising SEQ ID NO:2. Claim 13 describes the amplified DNA as one that hybridizes under stringent conditions to nucleotides 557 to 1171 of SEQ ID NO:1, which is 70% homologous to nucleotides 557 to 1171 of SEQ ID NO:1 and codes for a protein that confers L-homoserine resistance to the bacteria. Claim 17 describes the DNA as one that is obtainable by mutating nucleotides 557 to 1171 of SEQ ID NO:1 and codes for a protein that confers L-homoserine resistance to the bacteria.

In contrast, Zakataeva et al is an abstract publication but does not describe any sequence whatsoever. Therefore, the pending claims are not obvious or anticipated by Zakataeva et al and as such withdrawal of the rejections under 35 U.S.C. § 102(b) or under 35 U.S.C. § 103(a) is requested.

Turning to the rejections under 35 U.S.C. § 103(a) over Zakataeva et al combined with Daniels et al and Debabov et al (U.S. Patent 5,538,873), Applicants submit that this rejection is not tenable for the following reasons.

Daniels et al does not teach a nucleotide sequence of SEQ ID NO:1 nor the DNA encoding the protein-SEQ ID NO:2. Debabov merely describes the desire of producing amino acids. However, when these two publications are combined with Zakataeva, there is still no description or suggestion for SEQ ID NO:1 or SEQ ID NO:2. Therefore, Claim 8 and the claims dependent on Claim 8 cannot be obvious in view of this combination of prior art.

In a similar manner, Claims 13-20 are also not obvious in view of the combination of prior art for the following reasons.

"To establish prima facie obviousness of a claimed invention, all the claim limitations must be taught or suggested by the prior art." (MPEP §2143.03 citing *In re Royka*, 490 F.2d 981, 180 USPQ 580 (CCPA 19740)). Here, Daniels et al does not describe a protein or DNA encoding a protein that that has the ability to impart homoserine resistance as required for the protein encoded by the DNA in Claims 13-20. This is supported by the present specification on page 7, lines 3-17:

> The nucleotide sequence shown in SEQ ID NO: 1 corresponds to a part of sequence complement to the sequence of GenBank accession number M87049. SEQ ID NO: 1 includes f138 (nucleotide numbers 61959-61543 of GenBank accession number M87049) which is a known but function-unknown ORF (open reading frame) present at 86 min on *E. coli* chromosome, and 5'-flanking and 3'-flanking regions thereof. **The f138, which had only 160 nucleotides in the 5'-flanking region, could not impart the resistance to homoserine**. No termination codon is present between the 62160 and 61959 of M87049 (upstream the ORF f138). Hence, the coding region is 201 bp longer. Thus the RhtB protein and the *rhtB* gene coding for the protein are novel. (emphasis added)

This f 138 regions is what Daniels et al describes and therefore, the sequence of Daniels could not confer homoserine resistance in the bacteria expressing that DNA. Since Daniels et al does not describe the DNA encoding the protein with this activity, combining Daniels with Zakataeva et al and Debabov does not provide the requisite description of suggestion for every limitation of Claims 13 to 20. Furthermore, nothing in the combination of descriptions is there a suggestion to identify the DNA and protein that confer homoserine resistance to the bacteria so as to produce amino acids.

In light of the above, withdrawal of this ground of rejection is requested.

The rejection of Claims 8-11 under the doctrine of obviousness-type double patenting over Claims 1-4 of U.S. Patent No. 6,303,348 is addressed by the Terminal Disclaimer filed herewith.

Applicants submit that the present application is now ready for allowance. Early notification of such allowance is kindly requested.

Respectfully submitted,

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